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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=8; day=14; hr=8; min=9; sec=16; ms=907;]

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Application No: 10539723 Version No: 2.0

Input Set:

Output Set:

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Finished: 2009-07-29 17:34:23.082
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 879 ms
Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 10
Actual SeqID Count: 10

Error code	Error Description
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<110> Bayer CropScience GmbH
Hoehne, Michaela
Frohberg, Claus
Landschuetze, Volker

<120> Plant cells and plants which synthesize a starch with an increased final viscosity

<130> 65084.000013

<140> 10539723

<141> 2005-06-20

<150> EP 02028530.0

<151> 2002-12-19

<150> PCT/EP03/14840

<151> 2003-12-19

<150> EP 03090275.3

<151> 2003-08-29

<160> 10

<170> PatentIn version 3.5

<210> 1

<211> 4167

<212> DNA

<213> Solanum tuberosum

<220>

<221> CDS

<222> (207)..(3899)

<300>

<301> Abel, G.J., Springer, F., Willmitzer, L. and Kossmann, J.

<302> Cloning and functional analysis of a cDNA encoding a novel 139 kDa

<303> Plant J.

<304> 10

<305> 6

<306> 981-991

<307> 1996

<308> X94400

<309> 1995-12-22

<313> (1)..(4167)

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<308> EMBL / X94400

<309> 1997-04-16

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gatgttctat ttgattctgt ggtgaacaag agtttacaa agaacattcc ttttctttt 180

tttcttgggtt cttgtgtggg tcagcc atg gat gtt cca ttt cca ctg cat aga 233
Met Asp Val Pro Phe Pro Leu His Arg
1 5

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Pro Leu Ser Cys Thr Ser Val Ser Asn Ala Ile Thr His Leu Lys Ile
10 15 20 25

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Lys Pro Phe Leu Gly Phe Val Ser His Gly Thr Thr Ser Leu Ser Val
30 35 40

caa tct tct tca tgg agg aag gat gga atg gtt act ggg gtt tca ttt 377
Gln Ser Ser Ser Trp Arg Lys Asp Gly Met Val Thr Gly Val Ser Phe
45 50 55

cca ttt tgt gca aat ctc tcg gga aga aga cgg aga aaa gtt tca act 425
Pro Phe Cys Ala Asn Leu Ser Gly Arg Arg Arg Arg Lys Val Ser Thr
60 65 70

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Thr Arg Ser Gln Gly Ser Ser Pro Lys Gly Phe Val Pro Arg Lys Pro

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Ser Gly Met Ser Thr Gln Arg Lys Val Gln Lys Ser Asn Gly Asp Lys			
90	95	100	105
gaa agt caa agt act tca aca tct aaa gaa tct gaa att tcc aac cag			569
Glu Ser Gln Ser Thr Ser Lys Glu Ser Glu Ile Ser Asn Gln			
110	115	120	
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Lys Thr Val Glu Ala Arg Val Glu Thr Ser Asp Asp Asp Thr Lys Val			
125	130	135	
gtg gtg agg gac cac aag ttt ctg gag gat gag gat gaa atc aat ggt			665
Val Val Arg Asp His Lys Phe Leu Glu Asp Glu Asp Glu Ile Asn Gly			
140	145	150	
tct act aaa tca ata agt atg tca cct gtt cgt gta tca tct caa ttt			713
Ser Thr Lys Ser Ile Ser Met Ser Pro Val Arg Val Ser Ser Gln Phe			
155	160	165	
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Val Glu Ser Glu Glu Thr Gly Gly Asp Asp Lys Asp Ala Val Lys Leu			
170	175	180	185
aac aaa tca aag aga tcg gaa gag agt gat ttt cta att gat tct gta			809
Asn Lys Ser Lys Arg Ser Glu Glu Ser Asp Phe Leu Ile Asp Ser Val			
190	195	200	
ata aga gaa caa agt gga tct cag ggg gaa act aat gcc agt agc aag			857
Ile Arg Glu Gln Ser Gly Ser Gln Gly Glu Thr Asn Ala Ser Ser Lys			
205	210	215	
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Gly Ser His Ala Val Gly Thr Lys Leu Tyr Glu Ile Leu Gln Val Asp			
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gtt gag cca caa caa ttg aaa gaa aat aat gct ggg aat gtt gaa tac			953
Val Glu Pro Gln Gln Leu Lys Glu Asn Asn Ala Gly Asn Val Glu Tyr			
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Lys Gly Pro Val Ala Ser Lys Leu Leu Glu Ile Thr Lys Ala Ser Asp			
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Val Glu His Thr Glu Ser Asn Glu Ile Asp Asp Leu Asp Thr Asn Ser			
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Phe Phe Lys Ser Asp Leu Ile Glu Glu Asp Glu Pro Leu Ala Ala Gly			
285	290	295	
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Thr Val Glu Thr Gly Asp Ser Ser Leu Asn Leu Arg Leu Glu Met Glu			
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ttg caa ggg atc aga tta ttt tgt ttt cca gag gtt gta aaa cct gat Leu Gln Gly Ile Arg Leu Phe Cys Phe Pro Glu Val Val Lys Pro Asp 330	335	340	345	1241
gaa gat gtc gag ata ttt ctt aac aga ggt ctt tcc act ttg aag aat Glu Asp Val Glu Ile Phe Leu Asn Arg Gly Leu Ser Thr Leu Lys Asn 350	355	360	1289	
gag tct gat gtc ttg att atg gga gct ttt aat gag tgg cgc tat agg Glu Ser Asp Val Leu Ile Met Gly Ala Phe Asn Glu Trp Arg Tyr Arg 365	370	375	1337	
tct ttt act aca agg cta act gag act cat ctc aat gga gat tgg tgg Ser Phe Thr Thr Arg Leu Thr Glu Thr His Leu Asn Gly Asp Trp Trp 380	385	390	1385	
tct tgc aag atc cat gtt ccc aag gaa gca tac agg gct gat ttt gtg Ser Cys Lys Ile His Val Pro Lys Glu Ala Tyr Arg Ala Asp Phe Val 395	400	405	1433	
ttt ttt aat gga caa gat gtc tat gac aac aat gat gga aat gac ttc Phe Phe Asn Gly Gln Asp Val Tyr Asp Asn Asn Asp Gly Asn Asp Phe 410	415	420	425	1481
agt ata act gtg aaa ggt ggt atg caa atc att gac ttt gaa aat ttc Ser Ile Thr Val Lys Gly Gly Met Gln Ile Ile Asp Phe Glu Asn Phe 430	435	440	1529	
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aaa gct gaa att gaa gct gac aga gca caa gca aag gaa gag gct gca Lys Ala Glu Ile Glu Ala Asp Arg Ala Gln Ala Lys Glu Glu Ala Ala 475	480	485	1673	
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cgt gat atc acg tgg tac ata gag cca agt gaa ttt aaa tgc gag gac Arg Asp Ile Thr Trp Tyr Ile Glu Pro Ser Glu Phe Lys Cys Glu Asp 510	515	520	1769	
aag gtc agg tta tac tat aac aaa agt tca ggt cct ctc tcc cat gct Lys Val Arg Leu Tyr Tyr Asn Lys Ser Ser Gly Pro Leu Ser His Ala 525	530	535	1817	

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tct att gtc aaa aag ctt gtt aaa tct gag aga ata gat ggt gat tgg Ser Ile Val Lys Lys Leu Val Lys Ser Glu Arg Ile Asp Gly Asp Trp 555 560 565	1913
tgg tat aca gag gtt gtt att cct gat cag gca ctt ttc ttg gat tgg Trp Tyr Thr Glu Val Val Ile Pro Asp Gln Ala Leu Phe Leu Asp Trp 570 575 580 585	1961
gtt ttt gct gat ggt cca ccc aag cat gcc att gct tat gat aac aat Val Phe Ala Asp Gly Pro Pro Lys His Ala Ile Ala Tyr Asp Asn Asn 590 595 600	2009
cac cgc caa gac ttc cat gcc att gtc ccc aac cac att ccg gag gaa His Arg Gln Asp Phe His Ala Ile Val Pro Asn His Ile Pro Glu Glu 605 610 615	2057
tta tat tgg gtt gag gaa gaa cat cag atc ttt aag aca ctt cag gag Leu Tyr Trp Val Glu Glu His Gln Ile Phe Lys Thr Leu Gln Glu 620 625 630	2105
gag aga agg ctt aga gaa gcg gct atg cgt gct aag gtt gaa aaa aca Glu Arg Arg Leu Arg Glu Ala Ala Met Arg Ala Lys Val Glu Lys Thr 635 640 645	2153
gca ctt ctg aaa act gaa aca aag gaa aga act atg aaa tca ttt tta Ala Leu Leu Lys Thr Glu Thr Lys Glu Arg Thr Met Lys Ser Phe Leu 650 655 660 665	2201
ctg tct cag aag cat gta gta tat act gag cct ctt gat atc caa gct Leu Ser Gln Lys His Val Val Tyr Thr Glu Pro Leu Asp Ile Gln Ala 670 675 680	2249
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ggt aaa cct gaa att tgg ttc aga tgt tca ttt aat cgc tgg act cac Gly Lys Pro Glu Ile Trp Phe Arg Cys Ser Phe Asn Arg Trp Thr His 700 705 710	2345
cgc ctg ggt cca ttg cca cct cag aaa atg tcg cct gct gaa aat ggc Arg Leu Gly Pro Leu Pro Pro Gln Lys Met Ser Pro Ala Glu Asn Gly 715 720 725	2393
acc cat gtc aga gca act gtg aag gtt cca ttg gat gca tat atg atg Thr His Val Arg Ala Thr Val Lys Val Pro Leu Asp Ala Tyr Met Met 730 735 740 745	2441
gat ttt gta ttt tcc gag aga gaa gat ggt ggg att ttt gac aat aag Asp Phe Val Phe Ser Glu Arg Glu Asp Gly Gly Ile Phe Asp Asn Lys 750 755 760	2489
agc gga atg gac tat cac ata cct gtg ttt gga gga gtc gct aaa gaa	2537

Ser Gly Met Asp Tyr His Ile Pro Val Phe Gly Gly Val Ala Lys Glu			
765	770	775	
cct cca atg cat att gtc cat att gct gtc gaa atg gca cca att gca			2585
Pro Pro Met His Ile Val His Ile Ala Val Glu Met Ala Pro Ile Ala			
780	785	790	
aag gtg gga ggc ctt ggt gat gtt gtt act agt ctt tcc cgt gct gtt			2633
Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala Val			
795	800	805	
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Gln Asp Leu Asn His Asn Val Asp Ile Ile Leu Pro Lys Tyr Asp Cys			
810	815	820	825
ttg aag atg aat aat gtg aag gac ttt cgg ttt cac aaa aac tac ttt			2729
Leu Lys Met Asn Asn Val Lys Asp Phe Arg Phe His Lys Asn Tyr Phe			
830	835	840	
tgg ggt ggg act gaa ata aaa gta tgg ttt gga aag gtg gaa ggt ctc			2777
Trp Gly Thr Glu Ile Lys Val Trp Phe Gly Lys Val Glu Gly Leu			
845	850	855	
tcg gtc tat ttt ttg gag cct caa aac ggg tta ttt tcg aaa ggg tgc			2825
Ser Val Tyr Phe Leu Glu Pro Gln Asn Gly Leu Phe Ser Lys Gly Cys			
860	865	870	
gtc tat ggt tgt agc aat gat ggt gaa cga ttt ggt ttc ttc tgt cac			2873
Val Tyr Gly Cys Ser Asn Asp Gly Glu Arg Phe Gly Phe Phe Cys His			
875	880	885	
gcg gct ttg gag ttt ctt ctg caa ggt gga ttt agt ccg gat atc att			2921
Ala Ala Leu Glu Phe Leu Leu Gln Gly Gly Phe Ser Pro Asp Ile Ile			
890	895	900	905
cat tgc cat gat tgg tct agt gct cct gtt gct tgg ctc ttt aag gaa			2969
His Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu Phe Lys Glu			
910	915	920	
caa tat aca cac tat ggt cta agc aaa tct cgt ata gtc ttc acg ata			3017
Gln Tyr Thr His Tyr Gly Leu Ser Lys Ser Arg Ile Val Phe Thr Ile			
925	930	935	
cat aat ctt gaa ttt ggg gca gat ctc att ggg aga gca atg act aac			3065
His Asn Leu Glu Phe Gly Ala Asp Leu Ile Gly Arg Ala Met Thr Asn			
940	945	950	
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Ala Asp Lys Ala Thr Thr Val Ser Pro Thr Tyr Ser Gln Glu Val Ser			
955	960	965	
gga aac cct gta att gcg cct cac ctt cac aag ttc cat ggt ata gtg			3161
Gly Asn Pro Val Ile Ala Pro His Leu His Lys Phe His Gly Ile Val			
970	975	980	985
aat ggg att gac cca gat att tgg gat cct tta aac gat aag ttc att			3209
Asn Gly Ile Asp Pro Asp Ile Trp Asp Pro Leu Asn Asp Lys Phe Ile			

990	995	1000	
ccg att ccg tac	acc tca gaa aac gtt	gtt gaa ggc aaa aca gca	3254
Pro Ile Pro Tyr	Thr Ser Glu Asn Val	Val Glu Gly Lys Thr Ala	
1005	1010	1015	
gcc aag gaa gct	ttg cag cga aaa ctt	gga ctg aaa cag gct gac	3299
Ala Lys Glu Ala	Leu Gln Arg Lys Leu	Gly Leu Lys Gln Ala Asp	
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Leu Pro Leu Val	Gly Ile Ile Thr Arg	Leu Thr His Gln Lys Gly	
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atc cac ctc att	aaa cat gct att tgg	cgc acc ttg gaa cgg aac	3389
Ile His Leu Ile	Lys His Ala Ile Trp	Arg Thr Leu Glu Arg Asn	
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Asp Arg Ala Arg	Leu Cys Leu Thr Tyr	Asp Glu Pro Leu Ser His	
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Pro Asn Gly Phe	Se		